

FIGURE 1A-1

1 M A L R R S M G R P G L P P L P L P P P R L G L L L A A L A S
 1 CGCCGATGG CGCTGAGCG GAGCATGGG CGCGCGGGG TCCCGCGCT CGCGTGGCG GGTCTGGCT GCTCTGGCTT
 33 L L L P E S A A G L K L M G A P V K L T V S Q G Q P V K L N C S
 101 CTCTGCTGCT CCGGAGTCC GCGCGGCGG GTCTGAAGCT CATGGGAGC CCGGTGAAGC TGACACTGTC TCAGGGGCG CCGGTGAAGC TCAACTGCAG
 66 V E G M E P D I Q W V K D G A V V Q N L D Q L Y I P V S E Q H W
 201 TGTGAGGG ATGGAGGAGC CTGACATCCA GTGGGTGAG GATGGGCTG TGTCCAGAA CTTGGACCAG TTCTACATCC CAGTCAGCGA GCAGCACTGG
 99 I G F L S L K S V E R S D A G R Y W C Q V E D G G E T E I S Q P V W
 301 ATCGGCTTC TCAGCCTGAA GTCACTGAG CGCTCTGAG CCGCGCGTA CTGGTGCCAG GTGAGGATG GGGGTGAAC CGAGATCTCC CAGCCAGTGT
 133 L T V E G V P F F T V E P K D L A V P P N A P F Q L S C E A V G P
 401 GGCTACGGT AGAAGGTGT CCATTTTCA CAGTGGAGCC AAGATCTG GCAGTGCCAC CCAATGCCCC TTCCAACTG TCTTGTGAGG CTGTGGGTCC
 166 P E P V T I V W W R G T T K I G G P A P S P S V L N V T G V T Q S
 501 CCCTGAACCT GTTACCATG TCTGGTGGG AGGAACCTAG AAGATCGGG GACCGCTCC CTCTCATCT GTTTAAATG TAACAGGGGT GACCCAGAGC
 199 T M F S C E A H N L K G L A S S R T A T V H L Q A L P A A P F N I T
 601 ACCATGTTTT CCTGTGAGC TCACAACCTA AAGGCGCTG CCTCTCTCG CACAGCCACT GTTACCTTC AAGCACTGCC TGCAGCCCC TTCAACATCA
 233 V T K L S S S N A S V A W M P G A D G R A L L Q S C T V Q V T Q A
 701 CCGTGACAA GCTTTCAGC AGCAACGCTA GTGTGGCTG GATGCCAGT GCTGATGCC GAGCTCTGCT ACAGTCTGCT ACAGTCTGAG TGACACAGGC
 266 P G G W E V L A V V V P V P P F T C L L R D L V P A T N Y S L R V
 801 CCCAGGAGC TGGGAAGTCC TGGCTGTTGT GGTCCCTGTG CCCCCCTTA CTGCTGCTG CCGGACCTG GTGCTGCCA CCAACTACAG CCTCAGGGTG
 299 R C A N A L G P S P Y A D W V P F Q T K G L A P A S A P Q N L H A I
 901 CGCTGTGCA ATGCTTGGG GCGCTCTCC TATGCTGACT GGTGCGCTT TCAGACCAAG GGTCTAGCCC CAGCCAGCG TCCCCAAAC CTCCATGCCA
 333 R T D S G L I L E W E E V I P E A P L E G P L G P Y K L S W V Q D
 1001 TCCGCACAGA TTCAGGCTC ATCTTGGAGT GGAAGAAGT GATCCCCGAG GCGCTTTGG AAGGCCCCCT GGGACCTTAC AAAGTCTCT GGGTCAAGA
 366 N G T Q D E L T V E G T R A N L T G W D P Q K D L I V R V C V S N
 1101 CAATGGAAC CAGGATGAGC TGACAGTGA GGGGACAGG GCAATTTGA CAGGCTGGA TCCCCAAAG GACCTGATCG TACGTGTGTG CGTCTCCAAT
 399 A V G C G P W S Q P L V V S S H D R A G Q Q G P P H S R T S W V P V
 1201 GCAGTGGCT GTGACCCCTG GAGTCAGCA CTGGTGTCT CTCTCATGA CCGTGAGGC CAGCAGGGCC CTCCTCAGC CCGCACATCC TGCGTACCTG
 433 V L G V L T A L V T A A A L A L I L L R K R R K E T R F G Q A F D
 1301 TGTCTCTGG TGTGCTAAG GCGCTGTGC CCGGCGCTC ATCCTGCTC GAAAGAGAGC GAAAGAGAGC CGGTTTGGG AACCTTTGA

FIGURE 1A-2

466 S V M A R G E P A V H F R A A R S F N R E R P E R I E A T L D S L
1401 CAGTGTATG GCCGGGGAG AGCCAGCCGT TCACTTCGG GCAGCCCGT CCTTCAATCG AGAAGGCC GAGCGCATCG AGGCCACATT GGACAGCTTG
499 G I S D E L K E K L E D V L I P E Q Q F T L G R M L G K G E F G S V
1501 GGCATCAGCG ATGAACATAA GGAANAACG GAGGATGTC TCATCCAGA GCAGCAGTTC ACCCTGGGCC GGATGTTGGG CAAAGGAGAG TTTGGTTTCAG
533 R E A Q L K Q E D G S F V K V A V K M L K A D I I A S S D I E E F
1601 TCGGGAGGC CCAGCTGAAG CAAGAGGATG GCTCCTTTGT GAAAGTGGCT GTGAAGATGC TGAAGCTGA CATCATGGCC TCAAGCGACA TTGAAGAGATT
566 L R E A A C M K E F D H P H V A K L V G V S L R S R A K G R L P I
1701 CCTCAGGAA GCAGCTTGCA TGAAGGATT TGACCATCCA CACGTGGCCA AACTTGTGG GGTAAAGCCTC CGAGCAGGG CTAAAGGCCG TCTCCCCATC
599 P M V I L P F M K H G D L H A F L L A S R I G E N P F N L P L Q T L
1801 CCCATGGTCA TCTTGGCCCTT CATGAAGCAT GGGGACCTGC ATGCCTTCCT GCTCGCCCTCC CGGATTGGGG AGAACCCCTT TAACCTACCC CTCCAGACCC
633 I R F M V D I A C G M E Y L S S R N F I H R D L A A R N C M L A E
1901 TGATCCGGTT CATGGTGGAC ATTGCCTGG GCATGGAGTA CCGAGCTCT CGGAACCTCA TCCACCGAGA CCTGGCTGCT CGGAATTGCA TGCTGGCAGA
666 D M T V C V A D F G L S R K I Y S G D Y Y R Q G C A S K L P V K W
2001 GGACATGACA GTGTGTGTGG CTGACTTCGG ACTCTCCCG AGATCTACA GTGGGACTA CTATCGTCAA GGCTGTGCT CCAAACCTGCC TGTCAAGTGG
699 L A L E S L A D N L Y T V Q S D V W A F G V T M W E I M T R G Q T P
2101 CTGGCCCTGG AGAGCCTGG CGACAACCTG TATACTGTGC AGAGTGACGT GTGGGCTTC GGGTGACCA TGTGGGAGAT CATGACACGT GGGCAGACGC
733 Y A G I E N A E I Y N Y L I G G N R L K Q P P E C M E D V Y D L M
2201 CATATGCTGG CATCGAAGC GCTGAGATT ACAACTACCT CATTTGGCGG AACCGCTGA AACAGCCTCC GGAGTGTATG GAGGACCTGT ATGATCTCAT
766 Y Q C W S A D P K Q R P S F T C L R M E L E N I L G Q L S V L S A
2301 GTACCACTGC TGGAGTGTG ACCCCAAGCA GCGCCGAGC TTTACTTGTG TCGAATGGA ACTGGAGAAC ATCTTGGGCC AGCTGTCTGT GCTATCTGCC
799 S Q D P L Y I N I E R A E E P T A G G S L E L P G R D Q P Y S G A G
2401 AGCCAGACC CTTATACAT CAACATCAG AGAGTGAAG AGCCACATGC GGGAGGCAGC CTGAGCTAC CTGGCAGGA TCAGCCCTAC AGTGGGCTG
833 D G S G M G A V G G T P S D C R Y I L T P G G L A E Q P G Q A E H
2501 GGGATGGCAG TGGCATGGG GCAGTGGTG GCACTCCAG TGACTGTGG TACATACTCA CCCCCGAGG GCTGGCTGAG CAGCCAGGGC AGGCAGAGCA
866 Q P E S P L N E T Q R L L L L Q Q G L L P H S S C O
2601 CCAGCAGAG AGTCCCTCA ATGAGACACA GAGGCTTTG CTGCTGCAGC AAGGGTACT GCCACACAGT AGCTGTTAGC CCACAGGCAG AGGCATCGG
2701 GGCCATTGG CCGGCTCTGG TGGCCACTGA GCTGGCTGAC TAAGCCCCGT CTGACCCAG CCCAGACAGC AAGGTGTGA GGCTCCTGTG GTAGTCCTCC
2801 CAAGCTGTGC TGGGAAGCCC GGACTGACCA ATTCACCCAA TCCCAGTTCT TCCTGCAACC ACTCTGTGGC CAGCCTGGCA TCAGTTTAGG CCTTGGCTTG

FIGURE 1A-3

2901 ATGGAAGTGG GCCAGTCCTG GTTGTCTGAA CCCAGGCAGC TGGCAGGAGT GGGGTGGTTA TGTTTCCATG GTTACCATGG GTGTGGATGG CAGTGTGGGG
3001 AGGGCAGGTC CAGCTCTGTG GGGCCCTACCC TCCTGCTGAG CTGCCCCCTGC TGCTTAAAGTG CATGCATTGA GCTGCCCTCCA GCCTGGTGGC CCAGCTATT
3101 CCACACTTGG GGTTTAAATA TCCAGGTGTG CCCCTCCAAG TCACAAAGAG ATGTCCTTGT AATATTCCCT TTTAGGTGAG GGTGGTAAG GGGTTGGTAT
3201 CTCAGGCTG AATCTTCACC ATCTTTCTGA TTCCGCACCC TGCCTACGCC AGGAGAAGTT GAGGGGAGCA TGCTTCCCCTG CAGCTGACCG GGTACACAAA
3301 AGGCATGCTG GAGTACCCAG CCTATCAGGT GCCCCTCTTC CAAAGGCAGC GTGCCGAGCC AGCAAGAGGA AGGGGTGCTG TGAGGCTTGC CCAGGAGCAA
3401 GTGAGGCCCG AGAGGAGTTC AGGAACCCCT CTCCATACCC ACAATCTGAG CACGCTACCA AATCTCAAAA TATCCTAAGA CTAACAAAGG CAGCTGTGTC
3501 TGAGCCCCAAC CCTTCTAAAC GGTGACCTTT AGTGCCAAC TCCCTCTCTAA CTGGACAGCC TCTTCTGTCC CAAGTCTCCA GAGAGAAATC AGGCTTGATG
3601 AGGGGGAATT C

FIGURE 1B-1

1 1 C T C C G C C C A C C T C T C T C A G C G C T C G C G G G C G C G C G C G C G C A T G G T G C G C G T C G C C C C G A T G G C G C T G A G G C G G A G C A T G G G T G G C C G G G G C T C C G

14 P L L L A G L A S L L L P G S A A A G L K L M G A P V K M T V S Q G

101 C G C T G C T G C T G G C G G G A C T G G C T T C T C T G C T G C T C C C G G G T G T G C G C G C G C A G T A G C T C A T G G C G C G C C C A G T G A G A T G A C C G T G C T C A G G

48 Q P V K L N C S V E G M E D P D I H W M K D G T V V Q N A S Q V S

201 G G C A G C C A G T G A G C T C A A C T G C A G C G T G G A G G G A T G G A G A C C C T G A C A T C C A C T G G A T G A G A T G G C C A C G T G G T C C A G A T G C A A G C C A G T G T C

81 I S I S E H S W I G L L S L K S V E R S D A G L Y W C Q V K D G E

301 C A T C T C C A T C A G C G A G C A C A G C T G G A T T G G C T T A C T C A G C C T A A A G T C A G T G G A G C G T C T G A T G T G G C C T G T A C T G G T G C C A G T G A A G G A T G G G G A G

114 E T K I S Q S V W L T V E G V P F F T V E P K D L A V P P N A P F Q

401 G A A C C A A G A T C T C A G T C A G T A T G G C T C A G T G C G A G T G T G C C A T T C T T C A C A G T G G A C C A A A A G A T C T G G C G G T G C C A C C C A A T G C C C T T T T C

148 L S C E A V G P P E P V T I Y W W R G L T K V G G P A P S P S V L

501 A G C T G T C T T G T G A G G C T G G T C C T C C A G A A C C G T N A C C A T T A C T G G T G G A G A G A C T C A C T A A G T T G G G G A C C T T G C C C T C T C C T G T T T T

181 N V T G V T Q R T E F S C E A R N I K G L A T S R P A I V R L Q A

601 A A A T G T G A C A G A G T G A C C A G C G C A G A G T T T T C T T G T G A G C C C G A C A T A A A A G C C T G G C A C T T C C G A C C A G C C A T T G T T G C C T T C A A G C A

214 P P A A P F N T T V T T I S S Y N A S V A W V P G A D G L A L L H S

701 C G C C T G C A G C T C C T T T C A A C A C C A G A T A C A C A G A T C C A G C T A C A A C G T A G C G T G G T G C C A G T G C T G A C G C C T A G C T C T G T G C A T T

248 C T V Q V A H A P G E W E A L A V V V P V P P F T C L L R N L A P

801 C C T G T A C T G T A C A G T G G C A C A G C C C C A G A G A A T G G A G C C C T T G C T G T T G G T T C C T G T G C C A C C T T T T A C C T G C C T G T G C G A A C T T G G C C C C

281 A T N Y S L R V R C A N A L G P S P Y G D W V P F Q T K G L A P A

901 T G C C A C C A C T A C A G C C T T A G G T G C G C T G T G C C A A T G C C T T G G C C C T T C T C C C T A C G G C G A C C C T T T C A G A C C C C A A A G G G C C T A G C C C A G C C

314 R A P Q N F H A I R T D S G L I L E W E E V I P E D P G E G P L G P

1001 A G A G C T C C T C A G A A T T T C C A T G C C A T C G T A C C G A C T C A G C C T T A C C T G G A A T G G A A G A G T G A T T C C T G A A G A C C C T G G G A A G C C C C C T A G G A C

348 Y K L S W V Q E N G T Q D E L M V E G T R A N L T D W D P Q K D L

1101 C T T A T A G C T G T C T G G T C C A A G A A A T G G A C C C A G A T G A G T G A T G T G G A A G G A C C A G G C C C A A T C T G A C C G A C T G G G A T C C C C A G A A G G A C C T

381 I L R V C A S N A I G D G P W S Q P L V V S S H D H A G R Q G P P

1201 G A T T T T G C G T G T G T G C C T C C A A T G C A A T T G T G A T G G C C C T G G A G T C A G C C A C T G G T G G T G T C T T C T C A T G A C C A T G C A G G A G G C A G G C C C T C C C

414 H S R T S W V P V V L G V L T A L I T A A A L A L I L L R K R R K E

1301 C A C A G C C G C A C A T C C T G G T G C C T G T G G T C T G G G C G T G C T A C C G C C C T G A T C A C A G C T G C T G C C T T G G C C T C A T C C T G C T T C G G A A G A G A C G C A A G G

448 T R F G Q A F D S V M A R G E P A V H F R A A R S F N R E R P E R

1401 A G A C G C G T T C G G G C A A G C C T T T G A C A G T T C A T G G C C G A G G G A G C C A G T G T A C T T C C G G G A G C C C G A T C T T T C A A T C G A G A A A G C C T G A A C G

FIGURE 1B-2

481 I E A T L D S L G I S D E L K E K L E D V L I P E Q Q F T L G R M
1501 CATTGAGGCC ACATTGGATA GCCTGGGCAT CAGCGATGAA TTGAAGGAAA AGTGGGAGGA TGCTCTCATT CCAGAGCAGC AGTTCACCTT CGGTCCGGATG
514 L G K G E F G S V R E A Q L K Q E D G S F V K V A V K M L K A D I I
1601 TTGGCAAG GAGACTTGG ATCAGTGGG GAAGCCAGC TAAAGCAGGA AGATGGCTCC TTGCTGAANG TGCGATGAA GATGCTGAAA GGTGACATCA
548 A S S D I E E F L R E A A C M K E F D H P H V A K L V G V S L R S
1701 TTGCTCAAG CGACATAGAA GTGTTCTCC GGGAGCAGC TTGCATGAAG GAGTTGACC ATCCACACCT GGCCAAGCTT GTTGGGGTGA GCCTCCGGAG
581 R A K G R L P I P M V I L P F M K H G D L H A F L L A S R I G E N
1801 CAGGCTAAA GGTCTCTCC CCATTCCCAT GGTATCCTG CCCTTCATGA AACATGGAGA CTTCACAGCC TTCTGTCTG CCTCCCGAAT CGGGGAGAAC
614 P F N L P L Q T L V R F M V D I A C G M E Y L S S R N F I H R D L A
1901 CCTTTAACC TGCCCTGCA GACCTGGTC CGGTCATGG TGGACATTGC CTGTGGCATG GAGTACCIGA GCTCCCGNA CTTTCATCCAC CGAGACCTAG
648 A R N C M L A E D M T V C V A D F G L S R K I Y S G D Y Y R Q G C
2001 CAGCTCGGAA TTGCATGCTG GCCGAGGACA TGACAGTGTG TGTGGCTGAT TTGGACTCT CTGCGAATAT CTATAGCGGG GACTATTATC GTGAGGGCTG
681 A S K L P V K W L A L E S L A D N L Y T V H S D V W A F G V T M W
2101 TGCCTCCAAA TTGCCCTCA AGTGGCTGC CTTGGAGAGC TTGGCTGACA ACTGTATATAC TGTACACAGT GATGTGTGG CCTTGGGGT GACCATGTGG
714 E I M T R G Q T P Y A G I E N A E I Y N Y L I G G N R L K Q P P E C
2201 GAGATCATGA CTCGTGGCA GACCCATAT GCTGGCATG AAAATGCTGA GATTACAACT TACCTCATG GGGGAACCG CCTGAAGCAG CCTCCGAGT
748 M E E V Y D L M Y Q C W S A D P K Q R P S F T C L R M E L E N I L
2301 GCATGAGGA AGTGTATGAT CTCATGTACC AGTGTGGAG CCGCGACCCC AAGCAGGCC CAAGCTTCAC GTGTCTGGA ATGGAACCTG AGAACATTCT
781 G H L S V L S T S Q D P L Y I N I E R A E Q P T E S G S P E L H C
2401 GGGCACCTG TCTGTCTGT CCACAGCCA GGACCCCTTG TACATCAACA TTGAGAGAGC TGAGCAGCT ACTGAGAGTG GCAGCCCTGA GCTGCACTGT
814 G E R S S S E A G D G S G V G A V G G I P S D S R Y I F S P G G L S
2501 GGAGAGCGAT CCAGCAGGA GGCAGGGGAC GGCAGTGGG TGGGGGAGT AGGTGGCATC CCCAGTACT CTGGGTACAT CTTACAGCCC GGAGGGCTAT
848 E S P G Q L E Q Q P E S P L N E N Q R L L L Q Q G L L P H S S C
2601 CCGAGTCACC AGGCAGCTG GAGCAGCAGC CAGAAAGCCC CCTCAATGAG AACAGAGCC TGTGTGTCT GCAGCAAGGG CTACTGCCTC ACAGTAGCTG
881 O
2701 TTAACCTCA GGCAGAGGA AGTTGGGGC CCTGGCTCTG CTGACCGCTG CAGGCCAG TCTGATACA GCCCAGCAG CAAGGTATGG
2801 AGGCTCCTGT GGTAGCCCTC CCAAGCTGTG TGGGGCCTGG ACGGACCAAA TTGCCCCATC CCAGTTCTTC CTGCAGCCG TCTGGCCAGC CTGGCATCAG
2901 TTCAGCCCTT GGCTTAGAG AGGTAGCCA GAGCTGGTTG CCTGATGCA GGCAGTGGC AGGAGGGAG GGTGGCTATG TTTCATGGG TACCATGGGT
3001 GTGGATGCA GTAAGGAGG GTAGCAACAG CCTGTGGCC CCTACCCCTC TGGCTAGCT GCTCTACTT TAGTGCATG TTGGAGCCG CTGACGCTG
3101 GAATCAGCA CTGCCCCCA CACTTGGGC GAAATGGCC GTTTGGCCCT CTTAAGTCAC AAAGAGATGT CCATGTATTG TTCCCTTTTA GGTGATGATT

FIGURE 1B-3

3201 AGGAAGGGAT TGGCACACTT GGGTCCCTAA GCCCTATGGC AGGAATGGT GGGATATTCT CAGGTCTGAA TCCTCATCAT CTTCCTGATT CCCCACCCCTG
3301 CAAAGGCCCTG GAACCTGGCTG TGGGGCTCTG ACGCATGCTG AAGGACAAAA GGTACAGAG ATCCGACTTC AAAAGGCAGG GTCTGAGTCT GGCAGGTGGA
3401 GAGGTGCTAA GGGGCTGGCC CAGGAGTCAG GCATTTCAGG ACCCCTCCAA GCTTCTACAG TCTGTCTGAG CATGCTACCA AGCCCCCAGA TACCCCAAAA
3501 CTAACAGAGG CAGTTTTGTC TGAGCCCAGC CCTCCCACAT GATGACCCTT AGGTCTACCC TCCTCTCTAA ATGGACATCC TCGTTTGTC CAAGTCTCCA
3601 GAGAGACTAC TGATGGCTGA TGTGGGTAAG AAAAGTTCCA GGAACCAGGG CTGGGGTGA ACCAGGGCTG GGGTCGAGGC AGGCTCTTGG GCAGGCTCTT
3701 GCTGTTAGGA ACATTTCTAA GCTATTAACT TGCTGTTTCA AAACAAATAA AATTGAAACA TAAAGAATCA AAAAAAATAA AAAAA

FIGURE 2 -1

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1 GAATTCTCGA GTCGACGTTG GACTTGAAGG AATGCCAAGA GATGCTGCCC
51 CCACCCCCTT AGGCCCCGAGG GATCAGGAGC TATGGGACCA GAGGCCCTGT
1 MetGlyPro GluAlaLeuSer
*****

101 CATCTTTACT GCTGCTGCTC TTGGTGGCAA GTGGAGATGC TGACATGAAG
8 SerLeuLe uLeuLeuLeu LeuValAlaS erGlyAspAl aAspMetLys
*****

151 GGACATTTTG ATCCTGCCAA GTGCCGCTAT GCCCTGGGCA TGCAGGACCG
24 GlyHisPheA spProAlaLy sCysArgTyr AlaLeuGlyM etGlnAspArg

201 GACCATCCCA GACAGTGACA TCTCTGCTTC CAGCTCCTGG TCAGATTCCA
41 ThrIlePro AspSerAspI leSerAlaSe rSerSerTrp SerAspSerThr

251 CTGCCGCCCG CCACAGCAGG TTGGAGAGCA GTGACGGGGA TGGGGCCTGG
58 AlaAlaAr gHisSerArg LeuGluSerS erAspGlyAs pGlyAlaTrp

301 TGCCCCGCAG GGTCCGTGTT TCCCAAGGAG GAGGAGTACT TGCAGGTGGA
74 CysProAlaG lySerValPh eProLysGlu GluGluTyrL euGlnValAsp

351 TCTACAACGA CTGCACCTGG TGGCTCTGGT GGGCACCCAG GGACGGCATG
91 LeuGlnArg LeuHisLeuV alAlaLeuVa lGlyThrGln GlyArgHisAla

401 CCGGGGGCCT GGGCAAGGAG TTCTCCCGGA GCTACCGGCT GCGTTACTCC
108 GlyGlyLe uGlyLysGlu PheSerArgS erTyrArgLe uArgTyrSer

451 CGGGATGGTC GCCGCTGGAT GGGCTGGAAG GACCGCTGGG GTCAGGAGGT
124 ArgAspGlyA rgArgTrpMe tGlyTrpLys AspArgTrpG lyGlnGluVal

501 GATCTCAGGC AATGAGGACC CTGAGGGAGT GGTGCTGAAG GACCTTGGGC
141 IleSerGly AsnGluAspP roGluGlyVa lValLeuLys AspLeuGlyPro

551 CCCCCATGGT TGCCCGACTG GTTCGCTTCT ACCCCCGGGC TGACCGGGTC
158 ProMetVa lAlaArgLeu ValArgPheT yrProArgAl aAspArgVal

601 ATGAGCGTCT GTCTGCGGGT AGAGCTCTAT GGCTGCCTCT GGAGGGATGG
174 MetSerValC ysLeuArgVa lGluLeuTyr GlyCysLeuT rpArgAspGly

651 ACTCCTGTCT TACACCGCCC CTGTGGGGCA GACAATGTAT TTATCTGAGG
191 LeuLeuSer TyrThrAlaP roValGlyGl nThrMetTyr LeuSerGluAla

701 CCGTGTACCT CAACGACTCC ACCTATGACG GACATACCGT GGGCGGACTG
208 ValTyrLe uAsnAspSer ThrTyrAspG lyHisThrVa lGlyGlyLeu

751 CAGTATGGGG GTCTGGGCCA GCTGGCAGAT GGTGTGGTGG GGCTGGATGA
224 GlnTyrGlyG lyLeuGlyGl nLeuAlaAsp GlyValValG lyLeuAspAsp

801 CTTTAGGAAG AGTCAGGAGC TCGGGTCTG GCCAGGCTAT GACTATGTGG
241 PheArgLys SerGlnGluL euArgValTr pProGlyTyr AspTyrValGly

851 GATGGAGCAA CCACAGCTTC TCCAGTGGCT ATGTGGAGAT GGAGTTTGAG
258 TrpSerAs nHisSerPhe SerSerGlyT yrValGluMe tGluPheGlu

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Figure 2-2

901	TTTGACCGGC	TGAGGGCCTT	CCAGGCTATG	CAGGTCCACT	GTAACAACAT
274	PheAspArgL	euArgAlaPh	eGlnAlaMet	GlnValHisC	ysAsnAsnMet
951	GCACACGCTG	GGAGCCCGTC	TGCCTGGCGG	GGTGGAATGT	CGCTTCCGGC
291	HisThrLeu	GlyAlaArgL	euProGlyGl	yValGluCys	ArgPheArgArg
1001	GTGGCCCTGC	CATGGCCTGG	GAGGGGGAGC	CCATGCGCCA	CAACCTAGGG
308	GlyProAl	aMetAlaTrp	GluGlyGluP	roMetArgHi	sAsnLeuGly
1051	GGCAACCTGG	GGGACCCCAG	AGCCCGGGCT	GTCTCAGTGC	CCCTTGGCGG
324	GlyAsnLeuG	lyAspProAr	gAlaArgAla	ValSerValP	roLeuGlyGly
1101	CCGTGTGGCT	CGCTTTCTGC	AGTGCCGCTT	CCTCTTTGCG	GGGCCCTGGT
341	ArgValAla	ArgPheLeuG	lnCysArgPh	eLeuPheAla	GlyProTrpLeu
1151	TACTCTTCAG	CGAAATCTCC	TTCATCTCTG	ATGTGGTGAA	CAATTCCTCT
358	LeuPheSe	rGluIleSer	PheIleSerA	spValValAs	nAsnSerSer
1201	CCGGCACTGG	GAGGCACCTT	CCCGCCAGCC	CCCTGGTGCC	CGCCTGGCCC
374	ProAlaLeuG	lyGlyThrPh	eProProAla	ProTrpTrpP	roProGlyPro
1251	ACCTCCCACC	AACTTCAGCA	GCTTGAGCT	GGAGCCCAGA	GGCCAGCAGC
391	ProProThr	AsnPheSerS	erLeuGluLe	uGluProArg	GlyGlnGlnPro
1301	CCGTGGCCAA	GCCCCAGGGG	AGCCCGACCG	CCATCCTCAT	CGGCTGCCTG
408	ValAlaLy	sProGluGly	SerProThrA	laIleLeuIl	eGlyCysLeu
1351	GTGGCCATCA	TCCTGCTCCT	GCTGCTCATC	ATTGCCCTCA	TGCTCTGGCG
424	ValAlaIleI	leLeuLeuLe	uLeuLeuIle	IleAlaLeuM	etLeuTrpArg
1401	GCTGCACTGG	CGCAGGCTCC	TCAGCAAGGC	TGAACGGAGG	GTGTTGGAAG
441	LeuHisTrp	ArgArgLeuL	euSerLysAl	aGluArgArg	ValLeuGluGlu
1451	AGGAGCTGAC	GGTTCACCTC	TCTGTCCCTG	GGGACACTAT	CCTCATCAAC
458	GluLeuTh	rValHisLeu	SerValProG	lyAspThrIl	eLeuIleAsn
1501	AACCGCCCAG	GTCCTAGAGA	GCCACCCCCG	TACCAGGAGC	CCCGGCCTCG
474	AsnArgProG	lyProArgGl	uProProPro	TyrGlnGluP	roArgProArg
1551	TGGGAATCCG	CCCCACTCCG	CTCCCTGTGT	CCCCAATGGC	TCTGCGTTGC
491	GlyAsnPro	ProHisSerA	laProCysVa	lProAsnGly	SerAlaLeuLeu
1601	TGCTCTCCAA	TCCAGCCTAC	CGCCTCCTTC	TGGCCACTTA	CGCCCGTCCC
508	LeuSerAs	nProAlaTyr	ArgLeuLeuL	euAlaThrTy	rAlaArgPro
1651	CCTCGAGGCC	CGGGCCCCCC	CACACCCGCC	TGGGCCAAAC	CCACCAACAC
524	ProArgGlyP	roGlyProPr	oThrProAla	TrpAlaLysP	roThrAsnThr
1701	CCAGGCCTAC	AGTGGGGACT	ATATGGAGCC	TGAGAAGCCA	GGCGCCCCGC
541	GlnAlaTyr	SerGlyAspT	yrMetGluPr	oGluLysPro	GlyAlaProLeu
1751	TTCTGCCCCC	ACCTCCCCAG	AACAGCGTCC	CCCATTATGC	CGAGGCTGAC
558	LeuProPr	oProProGln	AsnSerValP	roHisTyrAl	aGluAlaAsp

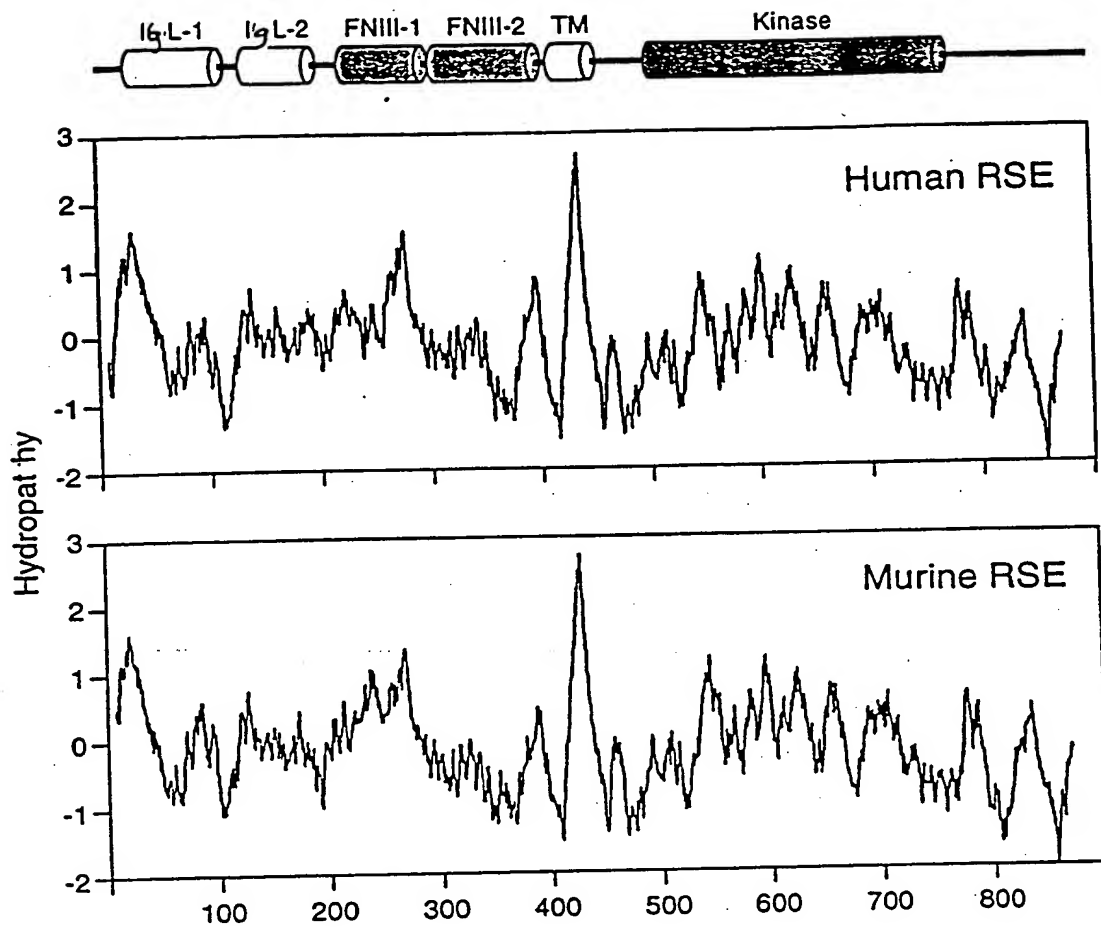
FIGURE 2-3

1801	ATTGTTACCC	TGCAGGGCGT	CACCGGGGGC	AACACCTATG	CTGTGCCTGC
574	IleValThrL	euGlnGlyVa	lThrGlyGly	AsnThrTyrA	laValProAla
1851	ACTGCCCCCA	GGGGCAGTCG	GGGATGGGCC	CCCCAGAGTG	GATTTCCCTC
591	LeuProPro	GlyAlaValG	lyAspGlyPr	oProArgVal	AspPheProArg
1901	GATCTCGACT	CCGCTTCAAG	GAGAAGCTTG	GCGAGGGCCA	GTTTGGGGAG
608	SerArgLe	uArgPheLys	GluLysLeuG	lyGluGlyGl	nPheGlyGlu
	<< <	
1951	GTGCACCTGT	GTGAGGTCTGA	CAGCCCTCAA	GATCTGGTCA	GTCTTGATTT
624	ValHisLeuC	ysGluValAs	pSerProGln	AspLeuVals	erLeuAspPhe
2001	CCCCCTTAAT	GTGCGTAAGG	GACACCCTTT	GCTGGTAGCT	GTCAAGATCT
641	ProLeuAsn	ValArgLysG	lyHisProLe	uLeuValAla	ValLysIleLeu
2051	TACGGCCAGA	TGCCACCAAG	AATGCCAGGA	ATGATTTCCT	GAAAGAGGTG
658	ArgProAs	pAlaThrLys	AsnAlaArgA	snAspPheLe	uLysGluVal
2101	AAGATCATGT	CGAGGCTCAA	GGACCCAAAC	ATCATTCGGC	TGCTGGGCGT
674	LysIleMetS	erArgLeuLy	sAspProAsn	IleIleArgL	euLeuGlyVal
2151	GTGTGTGCAG	GACGACCCCC	TCTGCATGAT	TACTGACTAC	ATGGAGAACG
691	CysValGln	AspAspProL	euCysMetIl	eThrAspTyr	MetGluAsnGly
2201	GCGACCTCAA	CCAGTTCCTC	AGTGCCACC	AGCTGGAGGA	CAAGGCAGCC
708	AspLeuAs	nGlnPheLeu	SerAlaHisG	lnLeuGluAs	pLysAlaAla
2251	GAGGGGGCCC	CTGGGGACGG	GCAGGCTGCG	CAGGGGGCCA	CCATCAGCTA
724	GluGlyAlaP	roGlyAspGl	yGlnAlaAla	GlnGlyProT	hrIleSerTyr
2301	CCCAATGCTG	CTGCATGTGG	CAGCCCAGAT	CGCCTCCGGC	ATGCGCTATC
741	ProMetLeu	LeuHisValA	laAlaGlnIl	eAlaSerGly	MetArgTyrLeu
2351	TGGCCACACT	CAACTTTGTA	CATCGGGACC	TGGCCACGCG	GAAGTGCCTA
758	AlaThrLe	uAsnPheVal	HisArgAspL	euAlaThrAr	gAsnCysLeu
2401	GTTGGGGAAA	ATTTACCAT	CAAAATCGCA	GACTTTGGCA	TGAGCCGGAA
774	ValGlyGluA	snPheThrIl	eLysIleAla	AspPheGlyM	etSerArgAsn
2451	CCTCTATGCT	GGGGACTATT	ACCGTGTGCA	GGGCCGGGCA	GTGCTGCCCA
791	LeuTyrAla	GlyAspTyrT	yrArgValGl	nGlyArgAla	ValLeuProIle
2501	TCCGCTGGAT	GGCCTGGGAG	TGCATCCTCA	TGGGGAAGTT	CACGACTGCG
808	ArgTrpMe	tAlaTrpGlu	CysIleLeuM	etGlyLysPh	eThrThrAla
2551	AGTGACGTGT	GGGCCTTTGG	TGTGACCCTG	TGGGAGGTGC	TGATGCTCTG
824	SerAspValT	rpAlaPheGl	yValThrLeu	TrpGluVall	euMetLeuCys
2601	TAGGGCCCAG	CCCTTTGGGC	AGCTCACCGA	CGAGCAGGTC	ATCGAGAACG
841	ArgAlaGln	ProPheGlyG	lnLeuThrAs	pGluGlnVal	IleGluAsnAla

FIGURE 2-4

2651	CGGGGGAGTT	CTTCCGGGAC	CAGGGCCGGC	AGGTGTACCT	GTCCCGGCCG
858	GlyGluPh	ePheArgAsp	GlnGlyArgG	lnValTyrLe	uSerArgPro
2701	CCTGCCTGCC	CGCAGGGCCT	ATATGAGCTG	ATGCTTCGGT	GCTGGAGCCG
874	ProAlaCysP	roGlnGlyLe	uTyrGluLeu	MetLeuArgC	ysTrpSerArg
2751	GGAGTCTGAG	CAGCGACCAC	CCTTTTCCCA	GCTGCATCGG	TTCCTGGCAG
891	GluSerGlu	GlnArgProP	roPheSerGl	nLeuHisArg	PheLeuAlaGlu
					>>>
2801	AGGATGCACT	CAACACGGTG	TGAATCACAC	ATCCAGCTGC	CCCTCCCTCA
908	AspAlaLe	uAsnThrVal			
2851	GGGAGTGATC	CAGGGGAAGC	CAGTGACACT	AAAACAAGAG	GACACAATGG
2901	CACCTCTGCC	CTTCCCCTCC	CGACAGCCCA	TCACCTCTAA	TAGAGGCAGT
2951	GAGACTGCAG	AAGCCCCTGT	CGCCCACCCA	GCTGGTCCTG	TGGATGGGAT
3001	CCTCTCCACC	CTCCTCTAGC	CATCCCTTGG	GGAAGGGTGG	GGAGAAATAT
3051	AGGATAGACA	CTGGACATGG	CCCATTGGAG	CACCTGGGCC	CCACTGGACA
3101	ACACTGATTC	CTGGAGAGGT	GGCTGCGCCC	CCAGCTTCTC	TCTCCCTGTC
3151	ACACACTGGA	CCCCACTGGC	TGAGAATCTG	GGGGTGAGGA	GGACAAGAAG
3201	GAGAGGAAAA	TGTTTCCTTG	TGCCTGCTCC	TGTACTTGTC	CTCAGCTTGG
3251	GCTTCTTCCT	CCTCCATCAC	CTGAAACACT	GGACCTGGGG	GTAGCCCCGC
3301	CCCAGCCCTC	AGTCACCCCC	ACTTCCCACC	TGCAGTCTTG	TAGCTAGAAC
3351	TTCTCTAAGC	CTATACGTTT	CTGTGGAGTA	AATATTGGGA	TTGGGGGGAA
3401	AGAGGGAGCA	ACGGCCCATA	GCCTTGGGGT	TGGACATCTC	TAGTGTAGCT
3451	GCCACATTGA	TTTTTCTATA	ATCACTTGGG	GTTTGTACAT	TTTTGGGGGG
3501	AGAGACACAG	ATTTTTACAC	TAATATATGG	ACCTAGCTTG	AGGCAATTTT
3551	AATCCCCTGC	ACTAGGCAGG	TAATAATAAA	GGTTGAGTTT	TCCACAAAAA
3601	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAA	

FIGURE 3



Signal Sequence

hRSE 1 M A L R - R S M G R P G L P P L P L P P P R L G L L L A A L A S L L L P S A A A - G L K L M G A
mRSE 1 M A L R - R S M G W P G L R P - - - - - L L L A G L A S L L L P G S A A A - G L K L M G A
hAXL 1 M A W R C P R M G R V P L A - - - - - W C L A L C G W A C H A P R G T O A E - E S P F V G N
mAXL 1 - - - - - M G R V P L A - - - - - W H L A L C C H G C A A H K D T O T E A G S P F V G N

* Ig-like Domain-1 *

hRSE 49 P V K L T V S Q G O P V K L N C S V E G M - E E P D I Q W V K D G A V V Q - - N L D Q L Y I P V S E
mRSE 39 P V K M T V S Q G O P V K L N C S V E G M - E D P D I H W M K D G T V V Q - - N A S Q V S I S I S E
hAXL 41 P G N I T G A R G L T G T L R C Q L O V Q G E P P E V H W L R D G O I L E L A D S T O T O V P L G E
mAXL 35 P G N I T G A R G L T G T L R C E L O V Q G E P P E V V W L R D G O I L E L A D N T O T O V P L G E

* Ig-like Domain-2 *

hRSE 96 - - - Q H W I G F - - L S L K S V E R S D A G R Y W C Q V E D G G E T E I S O P V H L T V E G V P P F
mRSE 86 - - - H S W I G L - - L S L K S V E R S D A G L Y W C Q V K D G E E T K I S Q S V H L T V E G V P P F
hAXL 91 D E O D D W I V Y S Q L R I T S L O L S D T G Q Y O C L V F L G H Q T F V S Q P G Y V G L E G L P Y
mAXL 85 D W Q D E W K V Y S Q L R I S A L O L S D A G E Y O C H V H L E G R T F V S Q P G F V G L E G L P Y

* FN Type III Domain *

hRSE 141 F T V E P K D L A V P P N A P F O L S C E A V G P P E P Y T I Y W H R G T T K I G - G P A P S P - S
mRSE 131 F T V E P K D L A V P P N A P F O L S C E A V G P P E P Y T I Y W H R G L T K V G - G P A P S P - S
hAXL 141 F L E E P E D R T Y A A N T P F N L S C Q A Q G P P E P Y D L L W L Q D A V P L A T A P G H G P O R
mAXL 135 F L E E P E D K A V P A N T P F N L S C Q A Q G P P E P Y T L L W L Q D A V P L A P Y T G H S S Q H

* FN Type III Domain *

hRSE 189 V L N V T G V T Q S T M F S C E A H N L K G L A S S R T A T V H L O A L P A A P F N I T V T K L S S
mRSE 179 V L N V T G V T Q R T E F S C E A R N I K G L A T S R P A I V R L O A P P A A P F N T T V T T I S S
hAXL 191 S L H V P G L N K T S S F S C E A H N A K G Y T T S R T A T I T V - - L P O O P R N L H L V S R O P
mAXL 185 S L Q T P G L N K T S S F S C E A H N A K G Y T T S R T A T I T V - - L P O R P H H L H V V S R O P

* FN Type III Domain *

hRSE 239 S N A S V A W M P G A D G R A L L O S C T V Q V T O A P G G H - - - - - E V L A V V V P
mRSE 229 Y N A S V A W V P G A D G L A L L H S C T V Q V A H A P G E W - - - - - E A L A V V V P
hAXL 239 T E L E V A W T P G L S G I Y P L T H C T L O A V L S D D G M G I O A G E P D P P E E P L T S O A S
mAXL 233 T E L E V A W T P G L S G I Y P L T H C N L O A V L S D D G V G I W L G K S D P P E D P L T L O V S

* FN Type III Domain *

hRSE 278 V P P F T C L L R D L V P A T N Y S L R V R C A N A L G P S P Y A D H V P F O T K G L A P A S A P O
mRSE 268 V P P F T C L L R N L A P A T N Y S L R V R C A N A L G P S P Y G D H V P F O T K G L A P A R A P O
hAXL 289 V P P H O L R L G S L H P H T P Y H I R V A C T S S Q G P S S W T H W L P V E T P E G V P L G P P E
mAXL 283 V P P H O L R L E K L L P H T P Y H I R I S C S S S Q G P S P W T H W L P V E T T E G V P L G P P E

* FN Type III Domain *

hRSE 328 N L H A I R T D S G L I L E W E E V I P E A P L E G P L G P Y K L S W V O D N G T O D E L T V E G T
mRSE 318 N F H A I R T D S G L I L E W E E V I P E D P G E G P L G P Y K L S W V O E N G T O D E L M V E G T
hAXL 339 N I S A T R N G S O A F Y H W O E - - P R A P L O G T L L G Y R L A Y - Q G O D T P E V L M D I G L
mAXL 333 N V S A M R N G S O V L V R W O E - - P R V P L O G T L L G Y R L A Y - R G O D T P E V L M D I G L

* Transmembrane Domain *

hRSE 378 R A N L T - G W D P O K D L I - V R V C V S - - N A V G C G P W S O P L V V - - - S S H D R A G O
mRSE 368 R A N L T - D W D P O K D L I - L R V C A S - - N A I G D G P W S O P L V V - - - S S H D H A G R
hAXL 386 R Q E V T L E L Q G D G S V S N L T V C V A A Y T A A G D G P W S L P V P L E A W R P G G A Q P V H
mAXL 380 T R E V T L E L R G D R P V A N L T V S V T A Y T S A G D G P W S L P V P L E P W R P G G G Q P L H

hRSE 465 DSYMA RGEPA VHFRA AARS FNRERPERIEATLDSLGISDELKEKLE DVLIIP
mRSE 455 DSYMARGEPA VHFRA AARS FNRERPERIEATLDSLGISDELKEKLE DVLIIP
hAXL 486 EPTVERGELVYRYRVKSSYSR - - - RTTEATLNSLGISEELKEKLRDVMVD
mAXL 480 EPTVERGELVYRYRVKSSYSR - - - RTTEATLNSLGISEELKEKLRDVMVD

Tyrosine Kinase Domain

hRSE 515 E Q O F T L G R M L G K G E F G S V R E A Q L K Q E D G S F V K V A V K M L K A D I I A S S D I E E
mRSE 505 E Q O F T L G R M L G K G E F G S V R E A Q L K Q E D G S F V K V A V K M L K A D I I A S S D I E E
hAXL 533 R H K V A L G K T L G E G E F G A V H E G Q L N Q D D - S I L K V A V K T M K I A I C T R S E L E
mAXL 527 R H K V A L G K T L G E G E F G A V H E G Q L N Q D D - S I L K V A V K T M K I A I C T R S E L E D

hRSE 565 F L R E A A C M K E F D H P H V A K L V G V S L R S R A K G R L P I P M V I L P F M K H G D L H A F
mRSE 555 F L R E A A C M K E F D H P H V A K L V G V S L R S R A K G R L P I P M V I L P F M K H G D L H A F
hAXL 582 F L S E A V C M K E F D H P H V M R L I G V C F O G S E R E S F P A P V V I L P F M K H G D L H S F
mAXL 576 F L S E A V C M K E F D H P H V M R L I G V C F O G S D R E G F P E P V V I L P F M K H G D L H S F

hRSE 615 L L A S R I G E N P F N L P L Q T L I R F M V D I A C G M E Y L S S R N F I H R D L A A R N C M L A
mRSE 605 L L A S R I G E N P F N L P L Q T L V R F M V D I A C G M E Y L S S R N F I H R D L A A R N C M L A
hAXL 632 L L Y S R L G D Q P V Y L P T Q M L V K F M A D I A S G M E Y L S T K R F I H R D L A A R N C M L N
mAXL 626 L L Y S R L G D Q P V F L P T Q M L V K F M A D I A S G M E Y L S T K R F I H R D L A A R N C M L N

hRSE 665 E D M T V C V A D F G L S R K I Y S G D Y Y R O G C A S K L P V K W L A L E S L A D N L Y T V Q S D
mRSE 655 E D M T V C V A D F G L S R K I Y S G D Y Y R O G C A S K L P V K W L A L E S L A D N L Y T V H S D
hAXL 682 E N H S V C V A D F G L S K K I Y N G D Y Y R O G R I A K M P V K W I A I E S L A D R V Y T S K S D
mAXL 676 E N H S V C V A D F G L S K K I Y N G D Y Y R O G R I A K M P V K W I A I E S L A D R V Y T S K S D

hRSE 715 V W A F G V T M H E I M T R G O T P Y A G I E N A E I Y N Y L I G G N R L K O P P E C M E D V Y D L
mRSE 705 V W A F G V T M H E I M T R G O T P Y A G I E N A E I Y N Y L I G G N R L K O P P E C M E E V Y D L
hAXL 732 V W S F G V T M H E I A T R G O T P Y P G V E N S E I Y D Y L R Q G N R L K O P A D C L D G L Y A L
mAXL 726 V W S F G V T M H E I A T R G O T P Y P G V E N S E I Y D Y L R Q G N R L K O P V D F L D G L Y S L

hRSE 765 M Y Q C W S A D P K Q R P S F T C L R M E L E N I L G O L S V L S A S O D P L Y I N I E R A E E P T
mRSE 755 M Y Q C W S A D P K O R P S F T C L R M E L E N I L G H L S V L S T S O D P L Y I N I E R A E O P T
hAXL 782 M S R C W E L N P O D R P S F T E L R E D L E N T L K A L P P A O E P D E I L Y V N M D E G G G Y P
mAXL 776 M S R C W E L N P R D R P S F A E L R E D L E N T L K A L P P A O E P D E I L Y V N M D E G G S H L

hRSE 815 A G G S L E L P G R D Q P Y S G A G D G S G M G A V G G T P S D C R Y I L T P G G L A E O P G O A E
mRSE 805 E S G S P E L H C G E R S S S E A G D G S G V G A V G G I P S D S R Y I F S P G G L S E S P G O L E
hAXL 832 E P P G A A G G A D P P T Q P D P K D S C S C L T A A E V H P A G R Y V L C P S T - T P S P A O P A
mAXL 826 E P R G A A G G A D P P T Q P D P K D S C S C L T A A D V H S A G R Y V L C P S T - A P G P T L S A

hRSE 865 H O P E S P L N E T Q R L L L L O O G L L P H S S C
mRSE 855 Q O P E S P L N E N Q R L L L L O O G L L P H S S C
hAXL 881 - D R G S P A A P G O - - - - E D G A - - - -
mAXL 875 - D R G C P A P P G O - - - - E D G A - - - -

FIGURE 5

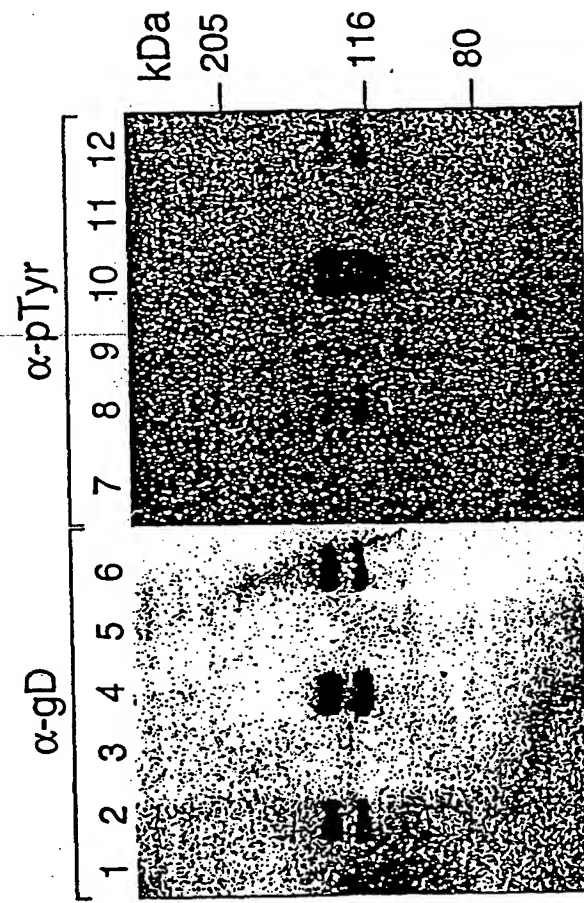
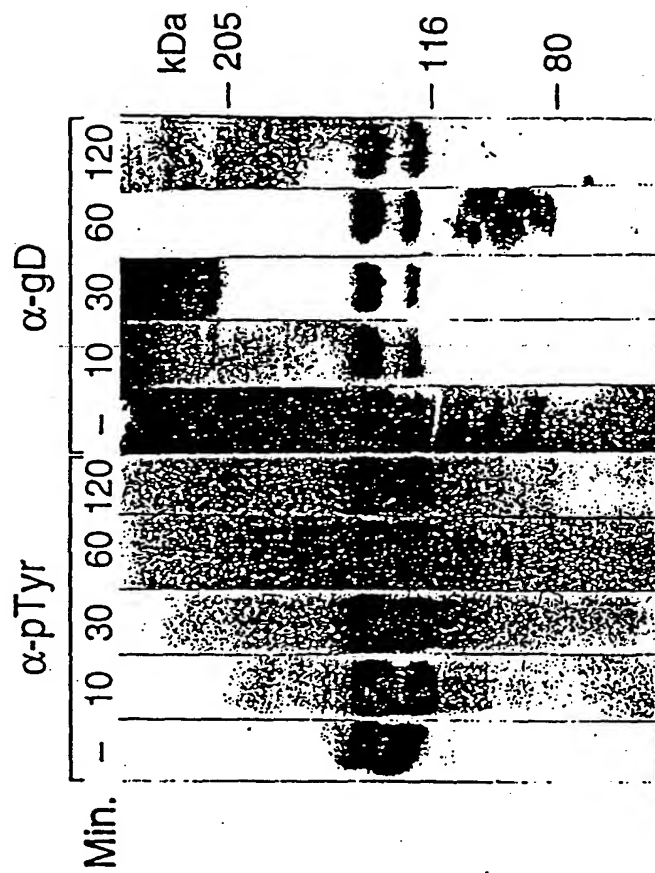


FIGURE 6



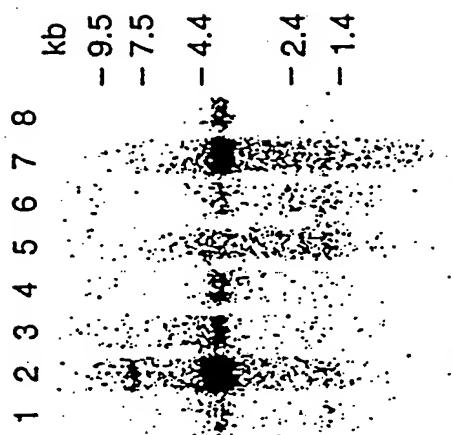


FIGURE 7A



FIGURE 7B

FIGURE 8 A

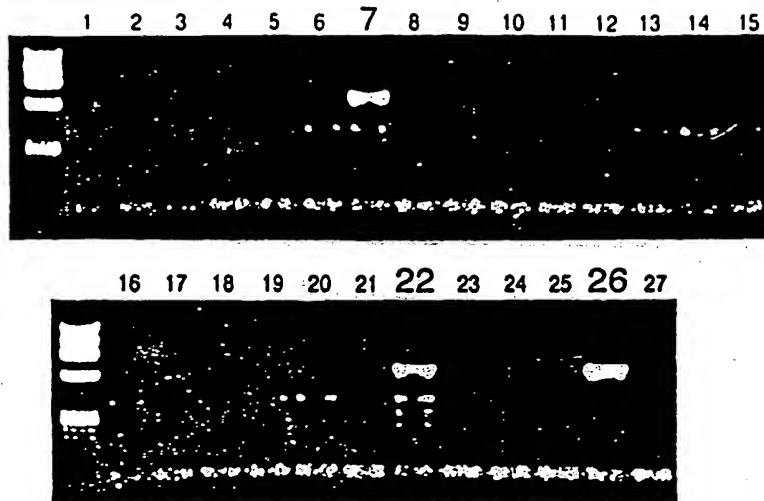


FIGURE 8B

CHROMOSOME CONTENT OF SOMATIC CELL HYBRID PANEL

[illegible]

FIGURE 9.

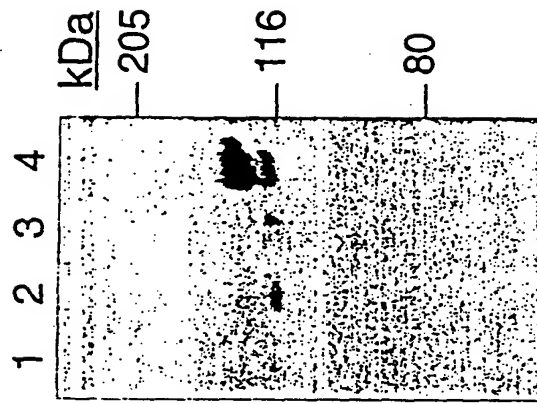


FIGURE 10A.

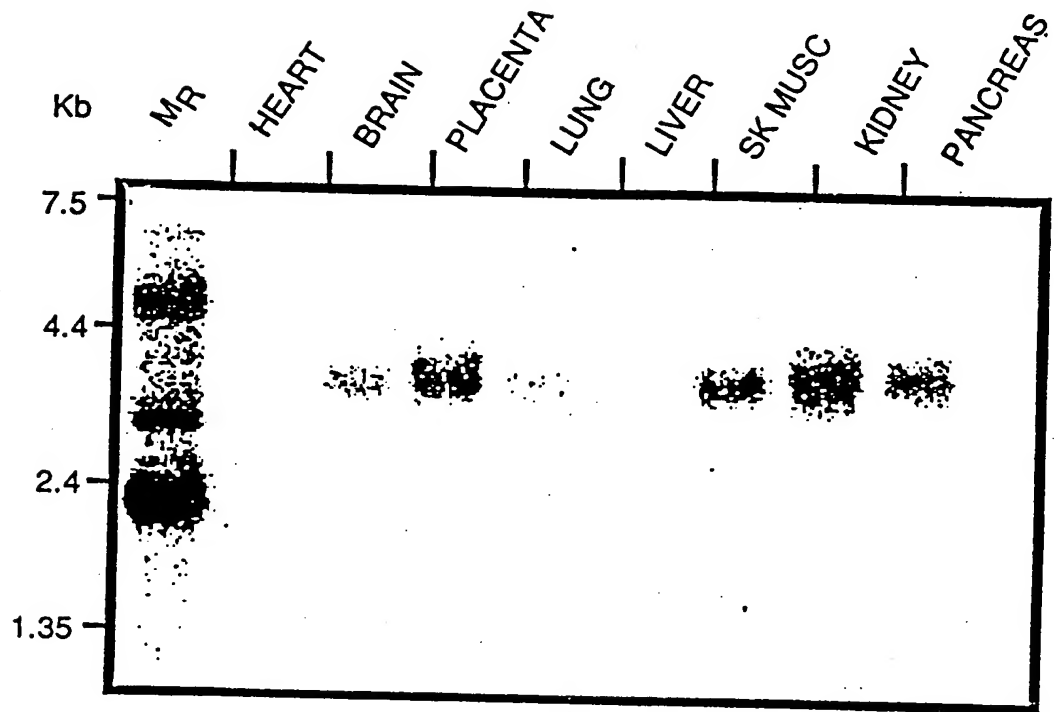


FIGURE 10 B.

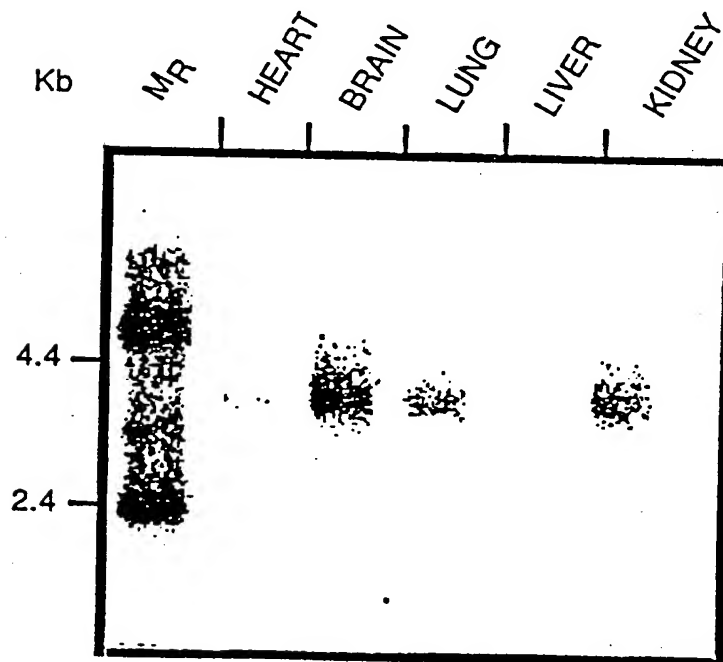


FIGURE 11A

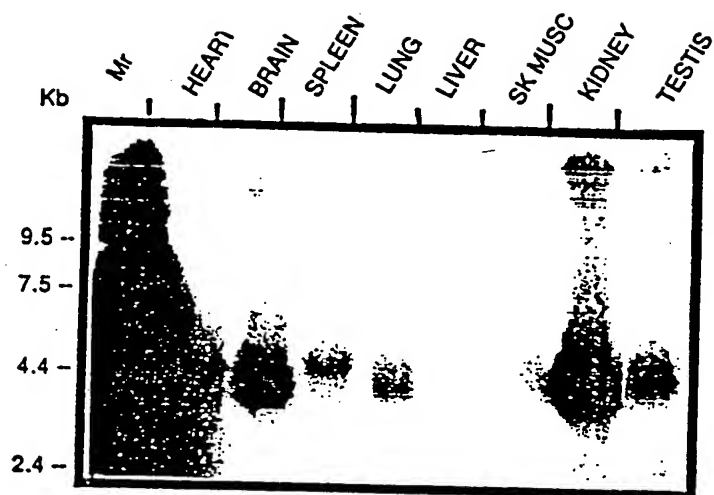


FIGURE 11B

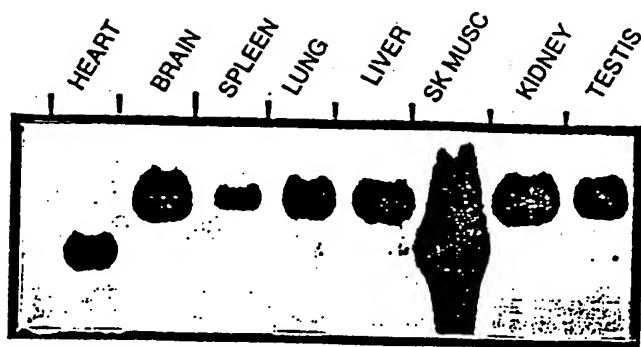


FIGURE 12A
HUMAN -ve STRAND

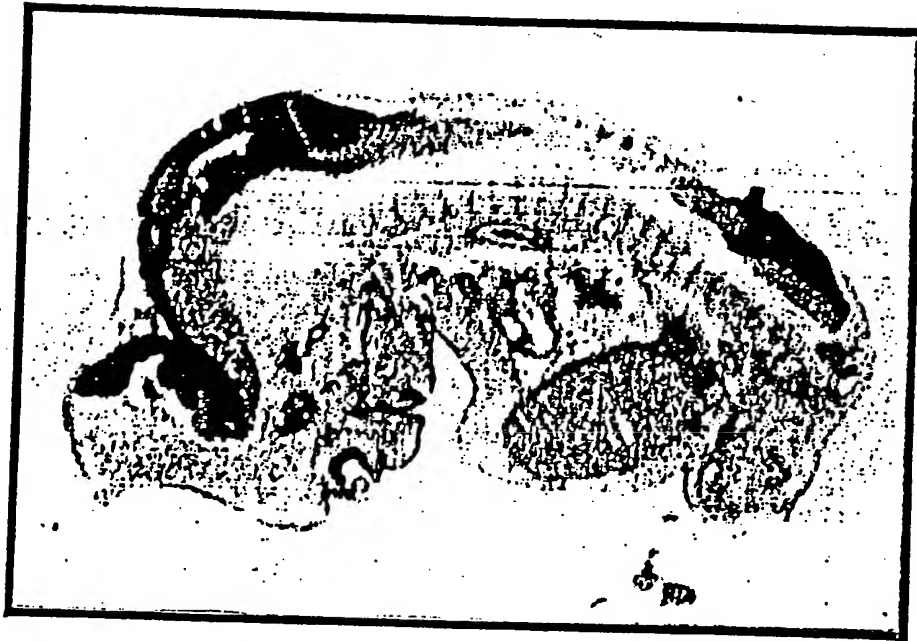


FIGURE 12B
MOUSE -ve STRAND



FIGURE 12C
MOUSE +ve STRAND

